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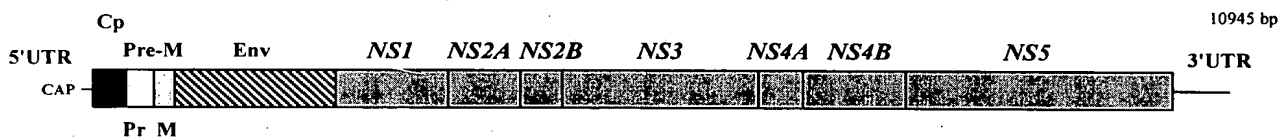
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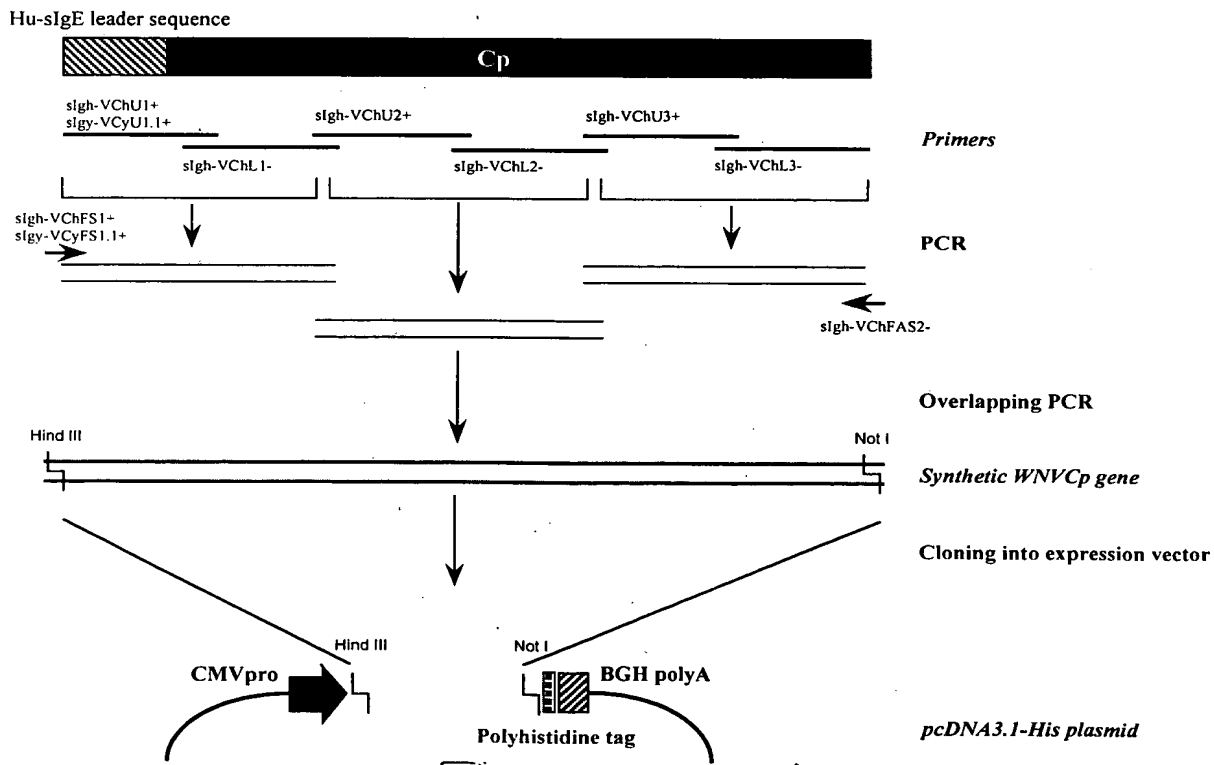
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Genomic organization of WNV-HNY1999



Cloning Strategy for WNV-HNY1999 Capsid Gene: pWNVh-DJY, pWNVy-DJY



pWNVh-DJY Cut site Map
Tuesday, September 5, 2000 2:09 PM

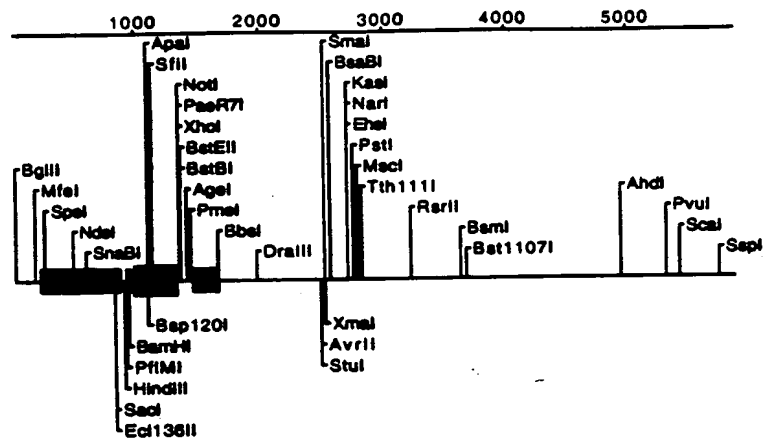


FIG. 2

pWNVh-DJY Cut Site Map
 Tuesday, September 5, 2000 2:09 PM

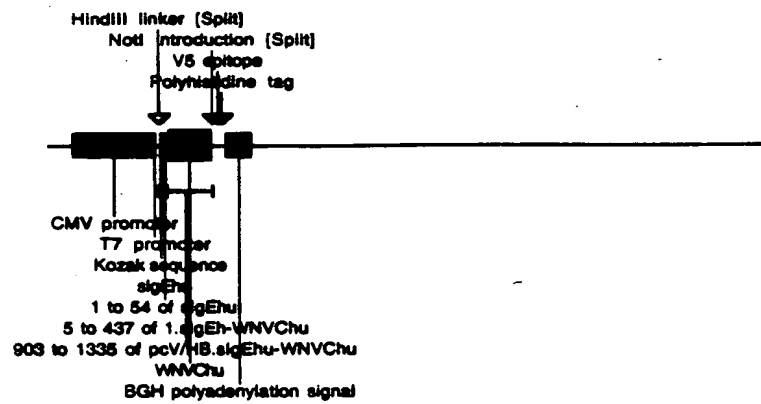


FIG. 3

Sequence Range: 1 to 5864

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>SpeI
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>NdeI
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610 620 630 640 650 660 670 680 690 700
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>Ecl136II
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>Kozak_sequence
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M D W T W I L F L V A A A T R V H S>
SIGEHU
S K K P G G P G K S>
WNVCHU
910 920 930 903 TO 1335 OF PCV/HB.SIGEHU-WNVCHU_0 980 990 1000>
10 20 30 5 TO 437 OF 1.SIGEH-WNVCHU_70 80 90 100>
10 10 1 TO 54 OF SIGEHU_40 50>

>PflMI
>BamHI
>T7_promoter
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>Kozak_sequence
>HindIII_linker (Split)
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M D W T W I L F L V A A A T R V H S>
SIGEHU
S K K P G G P G K S>
WNVCHU
910 920 930 903 TO 1335 OF PCV/HB.SIGEHU-WNVCHU_0 980 990 1000>
10 20 30 5 TO 437 OF 1.SIGEH-WNVCHU_70 80 90 100>
10 10 1 TO 54 OF SIGEHU_40 50>

>ApaI
>Bsp120I
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R A V N M L K R G M P R V L S L I G L K R A M L S L I D G K G P I>
WNVCHU
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110 120 130 5 TO 437 OF 1.SIGEH-WNVCHU_170 180 190 200>

>SfiI
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```

Fig 4

WNVCHU
1110 1120 1130 903 TO 1335 OF PCV/HB. SIGEHU-WNVCHU_70 1180 1190 1200
210 220 230 5 TO 437 OF 1.SIGEH-WNVCHU_270 280 290 300
1210 1220 1230 1240 1250 1260 1270 1280 1290 1300
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K H L L S F K K E L G T L T S A I N R R S S K Q K K R G G K T G I
WNVCHU
1210 1220 1230 903 TO 1335 OF PCV/HB. SIGEHU-WNVCHU_70 1280 1290 1300
310 320 330 5 TO 437 OF 1.SIGEH-WNVCHU_370 380 390 400
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>PaeR7I
>NotI
>XhoI
>BstBI
>NotI_introduction_[Split]
>V5_epitope
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CGGCACTACTAACCGGACTAGCGGTGCGCACCGCGCGCGGAGCTCCAGTGGGTAAAGCTTCCATTCCGATAGGATTGGGAGAGGAGCCAGAGCTAAGAT
A V M I G L I A S V G A
WNVCHU
903 TO 1335 OF PCV/HB. SIGEHU
5 TO 437 OF 1.SIGEH-WNVCHU
>AgeI
>PaeI
>Polyhistidine_tag
>BGH_polyadenylation_signal
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>StuI
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>XmaI
>BsaBI
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 >NarI
 >KasI
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 >Tth111I
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5610 5620 5630 5640 5650 5660 5670 5680 5690 5700
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GGGTGAGCAGCTGGGTGACTAGAAAGTCGAGAAATGAAGTGGTGCAGAAAGACCCACTCGTTTTTGTCTTCCGTTTTTACGGCGTTTTTTCCTTAT
5710 5720 5730 5740 5750 5760 5770 5780 5790 5800
GGGCGACACGGAATGTTGAATACTCATCTCTCTTTTCAATATTATTGAAGCATTATCAGGGTTATTGTCTCATGAGCGGATACATATTGAATG
CCCGCTGTGCTTTACAACTTATGAGTATGAGAAAGGAAAAAGTTATAATAACTTCGTAATAGTCCCAATAACAGAGTACTCGCTATGTATAAACTTAC
5810 5820 5830 5840 5850 5860
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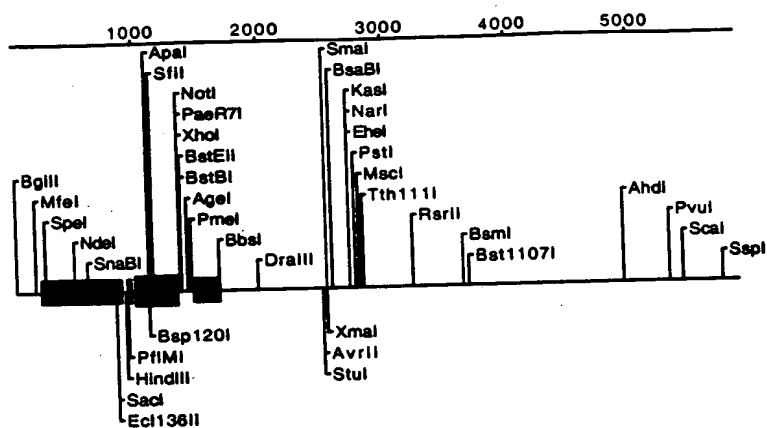


Fig. 5

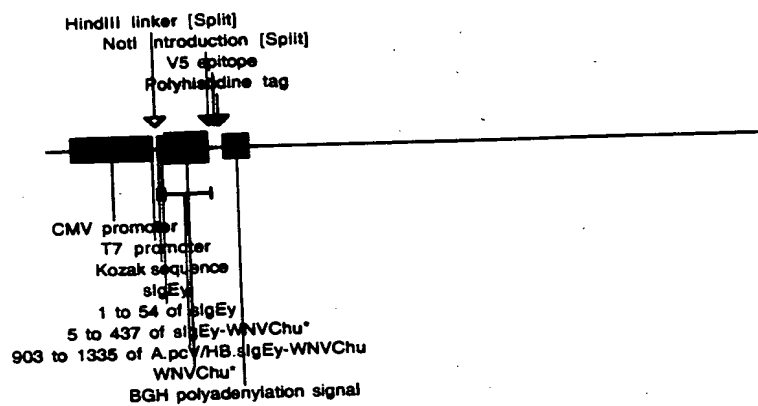


FIG. 6

Sequence Range: 1 to 5864

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>BglIII
10 20 30 40 50 60 70 80 90 100
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CTGCTAGCCCTCTAGAGGGCTAGGGGATACAGCTGAGAGTCATGTTAGACGAGACTACGGCTATCAATTCGGTCATAGACGAGGGACGAACACACAA

>MfeI
110 120 130 140 150 160 170 180 190 200
GGAGGTCGCTGAGTAGTCCGCGAGCAAAATTTAAGCTACAACAAGGCAAGCCTTGACCGACAATTGCATGAAGAACTCTGCTTAGGGTTAGGCGTTTTCGG
CCTCCAGCGACTCATACGCGCTCGTTTAAATTCGATGTTGTTCCGTTCCGAACGGCTGTTAAGTACTTCTTAGACGAATCCCAATCCGCAAAACGC

>SpeI
210 220 230 240 250 260 270 280 290 300
CTGCTTCGCGATGTACGGGCCAGATATACGGCTTGACATTGATTATTGACTAGTTATTAATAGTAATCAATTACGGGGTCATTAGTTTCATAGCCCATATA
GACGAAGCGCTACATGCCCCGTCTATATGCGCACTGTAATAAAGTATGATCAATAATTATCATTTAGTTAATGCCCCAGTAATCAAGTATCGGGTATAT

>CHV_promoter
310 320 330 340 350 360 370 380 390 400
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ACCTCAAGCGCAATGTATTGAATGCCATTTACCGGGCGGACCGACTGGCGGGTGTCTGGGGCGGGTAAGTGCAGTTATTACTGCATACAAAGGTATCA

>NdeI
410 420 430 440 450 460 470 480 490 500
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TTCGGTTATCCCTGAAAGGTAAGTGCAGTTACCCACCTGATAAATGCCATTTGACGGGTGAACCGTCAATGTAGTTACATAGTATACGGTTTCATGCGGG

>SnaBI
510 520 530 540 550 560 570 580 590 600
CCTATTGACGTCAATGACGGTAAATGGCCCGCTGGCATTATGCCAGTACATGACCTTATGGGACTTTCCTACTTGGCAGTACATCTACGTATTAGTCA
GGATAACTGCAGTTACTGCCATTTACCGGGCGGACCGTAAATACGGGTCTATGTAAGTAACTGCCGAAAGGTAAGCAACCGTCAATGTAGTGCATAATCAGT

610 620 630 640 650 660 670 680 690 700
TCGCTATTACCATGGTGTATGCGGGTTTGGCAGTACATCAATGGCGCTGGATAGCGGTTTGACTCACGGGGATTTCGAAGTCTCCACCCCATTTGACGTCAA
AGCGATAATGGTACCACCTACGCCAAAACCGTCTATGTTAGTTACCGCGACCTATCGCCAAACTGAGTGGCCCTACAGAGTGGGGTAACTGCAAGTT

710 720 730 740 750 760 770 780 790 800
TGGGAGTTTGTTTTGGCACAAAATCAACGGGACTTTCCAAAATGTCTGAACAACTCCGCCCATTTGACGCAAAATGGGCGGTAGGCGGTGACGGTGGGAG
ACCCCTAAACAAAACCGTGGTTTGTAGTTCCCTGAAAGGTTTACAGCATTTGTTGAGGCGGGTAACTGCGTTTACCGCCCATCCGCACATGCCACCTC

>SacI
810 820 830 840 850 860 870 880 890 900
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CAGATATATTCGTCTCGAGAGACCGATTGATCTCTTGGGTGACGAATGACCGAATAGCTTTAATTATGCTGAGTGATATCCCTCTGGGTTCCGACCGATCA

>HindIII
910 920 930 940 950 960 970 980 990 1000
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ATTCGAACGGCGGTGGTACCTAACCTGAACCTAGATAAAAAATCAACGACGACGATGATCTCAAGTAAGAAGATTTTTGGTCCACCGGGCGGTCTCTCG
M D W T W I L F L V A A A T R V H S>
SIGEY>
S K K P G G P G K S>
910 920 930 903 TO 1335 OF A. PCV/HB. SIGEY-WNVCHU_0 980 990 1000>
10 20 30 4.5 TO 437 OF SIGEY-WNVCHU* 70 80 90 100>
10 1 TO 54 OF SIGEY 40 50>

>Pf1MI
1010 1020 1030 1040 1050 1060 1070 1080 1090 1100
CGCGCCGTGAACATGCTGAAGCGCGGATGCCCGCGCTGCTGAGCCTGATTGGCTTGAAGCGCGCCATGCTGAGCCTGATCGAGCGGAAGGGCCCCATAC
GCGCGCACTTGTACGACTTCGCGCCCTACGGGGCGGACGACTCGGACTAACCGGACTTCGCGCGGTACGACTCGGACTAGCTGCCCTTCCCGGGTATG
R A V N M L K R G M P R V L S L I G L K R A M L S L I D G K G P I>
WNVCHU*
1010 1020 1030 903 TO 1335 OF A. PCV/HB. SIGEY-WNVCHU_70 1080 1090 1100>
110 120 130 1.5 TO 437 OF SIGEY-WNVCHU* 170 180 190 200>

>SfiI
1110 1120 1130 1140 1150 1160 1170 1180 1190 1200
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CGAAGCAGGACCGGGGACCGGAAGAGGCGAAGTGGCGGTAAACGGGGTGGCGCGCGGACGACTGGCGACCGCGCGCACTTGTGCTGGCGGTA
R F V L A L L A F F R P T A I A P T R A V L D R W R G V N K Q T A M>
```

FIG 7

4510 4520 4530 4540 4550 4560 4570 4580 4590 4600
GTGCTACAGAGTCTTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGGACAGTATTGGGTATCTGGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAG
CACGATGTCTCAAGAAGCTTCAACACCGGATGTATGCGGATGTGATCTTCTGTCTATAAACCATAGACGGGAGACGACTTCGGTCAATGGAAGCCTTTTTC
4610 4620 4630 4640 4650 4660 4670 4680 4690 4700
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TCAACCATCGAGAACTAGGCGGCTTGTTTGGTGGCGACCATCGCCACCAAAAAACAAACGTTGCTGCTCTAATGCGCGCTTTTTTTCTAGAGTTCTT
4710 4720 4730 4740 4750 4760 4770 4780 4790 4800
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CTAGGAACTAGAAAAAGATGCCCCAGACTGCGAGTCACTTGTCTTTGAGTGCAATTCCTTAAACAGTACTCTAATAGTTTTTCTAGAAAGTGATCT
4810 4820 4830 4840 4850 4860 4870 4880 4890 4900
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AGGAAAAATTAATTTTTTACTCAAAATTTAGTTAGATTTCATATATACTCAATTTGAACAGACTGTCAATGGTACGAATTAGTCACTCCGTGGATAGAG
4910 4920 4930 4940 4950 4960 4970 4980 4990 5000
>AhdI
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TCGCTAGACAGATAAAGCAAGTAGGTATCAACGGACTGAGGGGACGACATCTATTGATGCTATGCCCTCCCGAATGGTAGACGGGGTCAAGACGTTAC
5010 5020 5030 5040 5050 5060 5070 5080 5090 5100
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TATGGCGCTCTGGGTGCGAGTGGCGAGGTCTAAATAGTGGTTATTGGTGGTGGCGCTTCCCGCTCCGCTCTTACCAGGAGCTTGAATAGGCGGA
5110 5120 5130 5140 5150 5160 5170 5180 5190 5200
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GGTAGGTCAAGATAAATAACACGGCCCTTCGATCTATTTCATCAAGCGGTCAATTTATCAACCGGTTGCAACACGGTAAACGATGTCGCTAGCACACAG
5210 5220 5230 5240 5250 5260 5270 5280 5290 5300
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TGCGAGCAGCAAAACATACCGAAGTAAGTCGAGGCGAAGGGTGTAGTTCCGCTCAATGTACTAGGGGTACAACACGTTTTTTGCCCAATCGAGGAAG
5310 5320 5330 5340 5350 5360 5370 5380 5390 5400
>PvuII
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CCAGGAGGCTAGCAACAGTCTTCAATCAACCGCGCTCACAAATAGTGAGTACCAATACCGTCTGTGACGTATTAGAGAAATGACAGTACGGTAGGCATTCTA
5410 5420 5430 5440 5450 5460 5470 5480 5490 5500
>ScaI
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CGAAAAGACACTGACCACTCATGAGTTGGTTCAGTAAGACTCTTATCACATACGCGCTGGCTCAACGAGAACGGGCGCAGTTATGCCCTATTATGGCG
5510 5520 5530 5540 5550 5560 5570 5580 5590 5600
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CGGTGTATCGTCTTGAATTTTACAGGATAGTAACCTTTTGAAGAAGCCCGCTTTTGAGAGTTCTAGAAATGGCGACAACCTTAGGTCAAGCTACATT
5610 5620 5630 5640 5650 5660 5670 5680 5690 5700
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GGGTGAGCAGCTGGGTGACTAGAAAGTCGTAGAAAAATGAAGTGGTCGCAAAAGACCCACTGTTTTTGTCTTCCGTTTTACGGCGTTTTTCCCTTATT
5710 5720 5730 5740 5750 5760 5770 5780 5790 5800
>SspI
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5810 5820 5830 5840 5850 5860
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WNVCHU*
1110 1120 1130_903 TO 1335 OF A.PCV/HB.SIGBY-WNVCHU_70 1180 1190 1200
210 220 230 2_5 TO 437 OF SIGBY-WNVCHU* 270 280 290 300
1210 1220 1230 1240 1250 1260 1270 1280 1290 1300
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CTTCGTGGAGCAGCTGGAAGTCTTCCTCGACCCGCTGGGACTGGTCCGCGTAGTTGGCGGCGTCTGCTTCGTCTTCCTCGCGCCCGCTTCGGCGGTAA
K H L L S F K K E L G T L T S A I N R R S S K Q K K R G G K T G I
WNVCHU*
1210 1220 1230_903 TO 1335 OF A.PCV/HB.SIGBY-WNVCHU_70 1280 1290 1300
310 320 330 3_5 TO 437 OF SIGBY-WNVCHU* 370 380 390 400
>BstBII
|
|>PaeR7I
|>NotI |>XhoI |>BstBI
|>NotI_introduction_(Split) |>V5_epitope
1310 1320 1330 1340 1350 1360 1370 1380 1390 1400
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CGGCACTACTAACCGGACTAGCGGTGCGACCCGCGCGCGGAGCTCCAGTGGGTAAGCTTCCATTCCGATAGGGATTGGGAGAGGAGCCAGAGCTAAGAT
A V M I G L I A S V G A
903 TO 1335 OF A.PCV/HB.SIGBY-WNVCHU*
5 TO 437 OF SIGBY-WNVCHU*
>AgeI |>PmeI
|>Polyhistidine_tag |>BGH_polyadenylation_signal
1410 1420 1430 1440 1450 1460 1470 1480 1490 1500
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GCGCATGGCCAGTAGTAGTGGTAGTGAATCAAAATTTGGGCGACTAGTTCGGAGCTGACACGGAAGATCAACGGTCCGTAGACAACAACCGGGAGGGG
1510 1520 1530 1540 1550 1560 1570 1580 1590 1600
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1710 1720 1730 1740 1750 1760 1770 1780 1790 1800
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1810 1820 1830 1840 1850 1860 1870 1880 1890 1900
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>DraIII
1910 1920 1930 1940 1950 1960 1970 1980 1990 2000
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GCTAAATCAGGAATGCGGTGGAGCTGGGGTTTTTGAACCTAATCCCACTACCAAGTGCATCACCCTGATCGGGACTATCTGCCAAAAGCGGGAACT
2010 2020 2030 2040 2050 2060 2070 2080 2090 2100
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GCAACCTCAGGTGCAAGAAATATCACCCTGAGAACAGGTTTGACCTTGTGTGAGTTGGGATAGAGCCAGATAAGAAAACCTAAATATCTCCCTAAACCC
2110 2120 2130 2140 2150 2160 2170 2180 2190 2200
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2210 2220 2230 2240 2250 2260 2270 2280 2290 2300
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2310 2320 2330 2340 2350 2360 2370 2380 2390 2400
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>AvrII
|>StuI
2410 2420 2430 2440 2450 2460 2470 2480 2490 2500
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>SmaI
|>XmaI
2510 2520 2530 2540 2550 2560 2570 2580 2590 2600
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>EheI
>NarI
>KasI
2610 2620 2630 2640 2650 2660 2670 2680 2690 2700
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GCGGCGAACCACCTCTCGGATAAGCCGATAGTACCCGCTGTGTCTGTTAGCCGACGAGACTACGGCGGCACAAAGCCGACAGTCTCGCTCCCGCGGG
2710 2720 2730 2740 2750 2760 2770 2780 2790 2800
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>Tth111I
2810 2820 2830 2840 2850 2860 2870 2880 2890 2900
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CGACACGAGCTGCAACAGTGAATTCGCCCTTCCTTGACCGACGATTAACCGCTTACGGCGCCGCTCTAGAGGACAGTAGAGTGAACGAGGACGGCTCT
2910 2920 2930 2940 2950 2960 2970 2980 2990 3000
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3010 3020 3030 3040 3050 3060 3070 3080 3090 3100
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ATGAGCTACCTTTCGGCCAGAACAGCTAGTCTACTAGACCTGCTTCGTAGTTCGCCGAGCGGGTTCGGCTTGACAAGCGGTCCGAGTTCGCCGCGTAC
3110 3120 3130 3140 3150 3160 3170 3180 3190 3200
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>RsrII
3210 3220 3230 3240 3250 3260 3270 3280 3290 3300
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3310 3320 3330 3340 3350 3360 3370 3380 3390 3400
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3410 3420 3430 3440 3450 3460 3470 3480 3490 3500
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CGGTTTGGACGGTAGTGCTCTAAGCTAAGGTGCGCGCGGAAGATACTTTTCAACCCGAAGCCTTAGCAAAAGCGCTTCGGCGCGCTACTAGGAGTCT
3510 3520 3530 3540 3550 3560 3570 3580 3590 3600
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>BsmI
>Bst1107I
3610 3620 3630 3640 3650 3660 3670 3680 3690 3700
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3710 3720 3730 3740 3750 3760 3770 3780 3790 3800
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3810 3820 3830 3840 3850 3860 3870 3880 3890 3900
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3910 3920 3930 3940 3950 3960 3970 3980 3990 4000
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CCTCTCCGCCAAGCGATAACCCGCGAGAGGCGAAGGAGCGAGTGAAGTGAAGGCGAGCCAGCAAGCCGACGCGCTCGCATAGTCGAGTGAGTTT
4010 4020 4030 4040 4050 4060 4070 4080 4090 4100
GGCGGTAAATACGGTTATCCACAGAAATCAGGGGATAACGAGGAAGAAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAGAGCGCGGTTG
CCGCCATTATGCCAATAGGTGTCTTAGTCCCTATTGCGTCTTCTTGTACACTCGTTTTCGGTCTGTTTTCGGTCTTGGCATTTTTCGGCGCAAC
4110 4120 4130 4140 4150 4160 4170 4180 4190 4200
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GACCGCAAAAGGTATCCGAGGCGGGGAGCTGCTGTAGTGTTTTATGCTGCGAGTTCAGTCTCCACCGCTTTGGGCTGTCTGATATTTCTATGTTCC
4210 4220 4230 4240 4250 4260 4270 4280 4290 4300
CGTTTCCCGCTGGAAGCTCCCTCGTGCCTCTCCCTGTTCCGACCTTCCCGCTTACCGGATACCTGTTCGGCTTTCTCCCTTCGGGAAGCGTGGCGCTTC
GCAAGGGGGGACCTTCGAGGAGCAGCGAGAGGACAGGCTGGAGCGCGAAATGGCTATGACAGCGGGAAGAGGGAAGCCCTTCGACCGCGGAAG
4310 4320 4330 4340 4350 4360 4370 4380 4390 4400
TCAATGCTCAGCGCTGTAGGTATCTCAGTTTCGGTGTAGGTGCTGCTGCTCAAGCTGGGCTGTGTGACGAAACCCCGTTTCAGCCCGGACCGCTTCGCGCTTA
AGTTACGAGTGCACATCCATAGAGTCAAGCCACATCCAGCAAGCGAGGTTTCGACCGGACACAGTGTTCGGGGGCAAGTCGGGCTGGCGACGCGGAAT
4410 4420 4430 4440 4450 4460 4470 4480 4490 4500
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**³⁵S-Labelled *in vitro* Translated Products of
pWNVCh-DJY and pWNVcy-DJY**

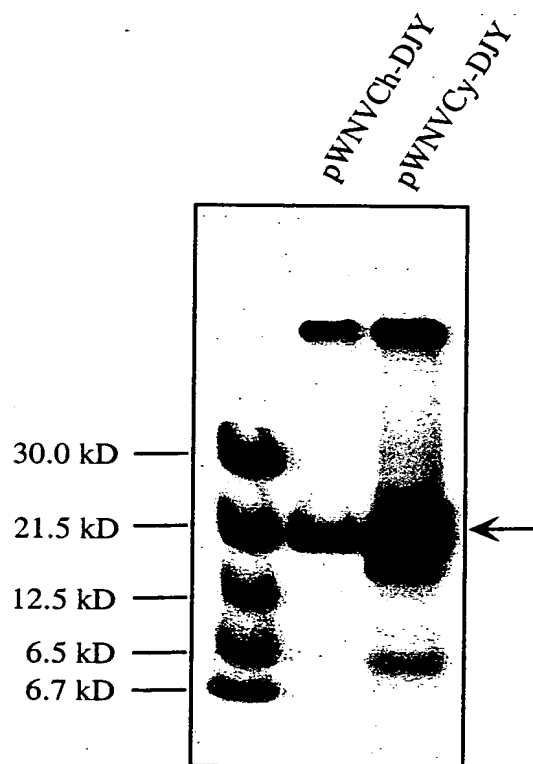


Fig 8

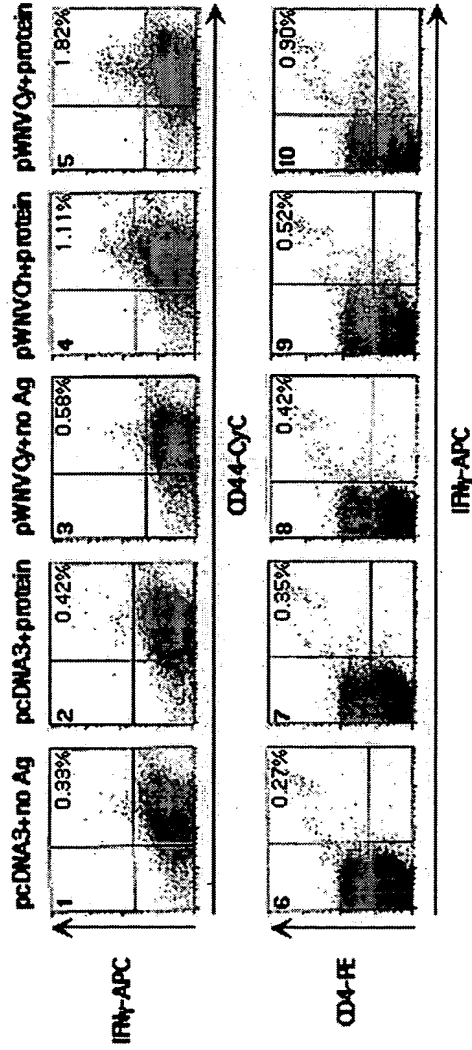
WNV Capsid (Cp) Peptides - Location and Sequences

WNV Cp Amino Acid Sequence	10	20	30	40	50	60	70	80	90	100	110	120
	MSKKPGGPGKSRVNNMLKRGMPRVLSLIGLKRAMLSLIDGKGPIRFVLALLAFFRFTATPTRAFLDWRGVNKGOTAMKHLISFKKELGTLTSAINRRSSQKKRGGKTGTIAVMIGLIASVGA											
Peptide Seq. Peptide Name	<div> <div>SKKPGGPGKSRVNNMLKRGMPR</div> <div>WNV-P1</div> </div> <div> <div>KRAMLSLIDGKGPIRFVLA</div> <div>WNV-P2</div> </div> <div> <div>TLTSAINRRSSQKKRGGKTGTI</div> <div>WNV-P3</div> </div>											

Fig. 9

FIGURE 10

Fig. 10



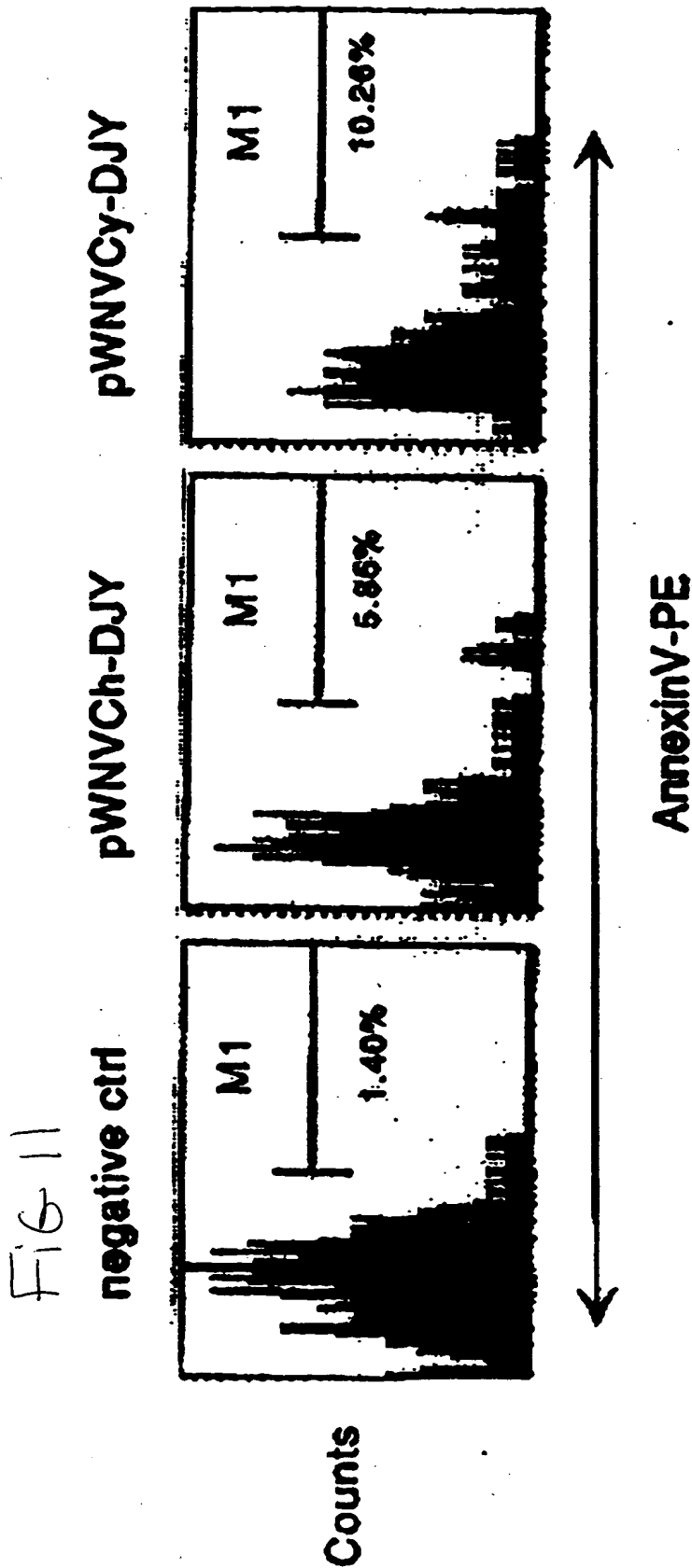


Fig. 12A

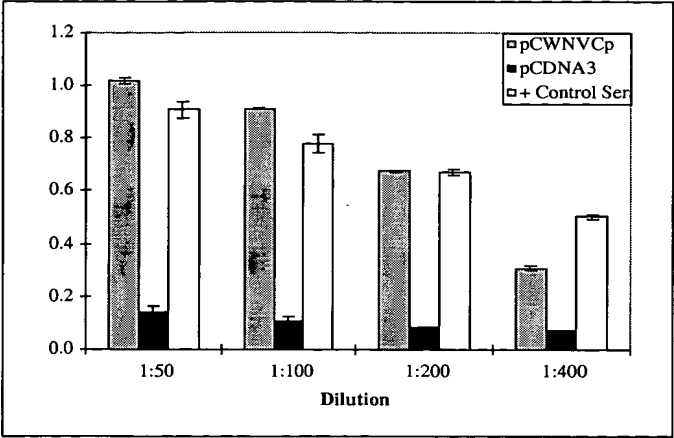


Fig. 12B

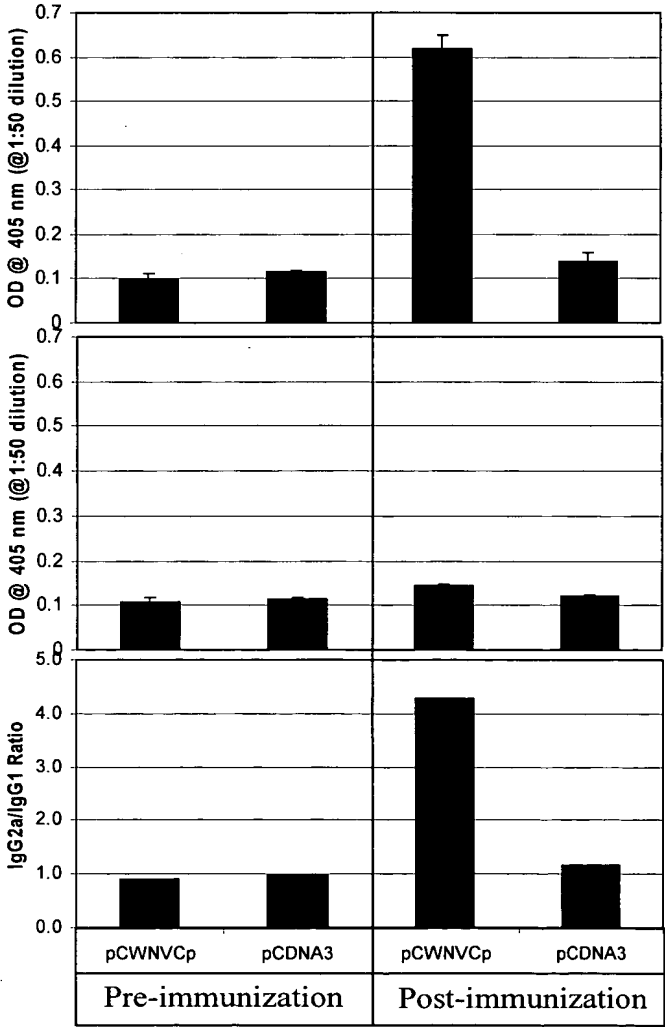
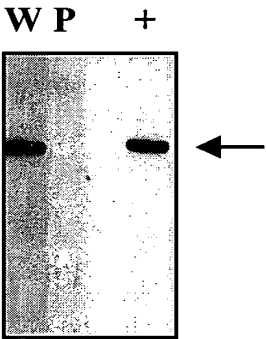


Fig. 12C



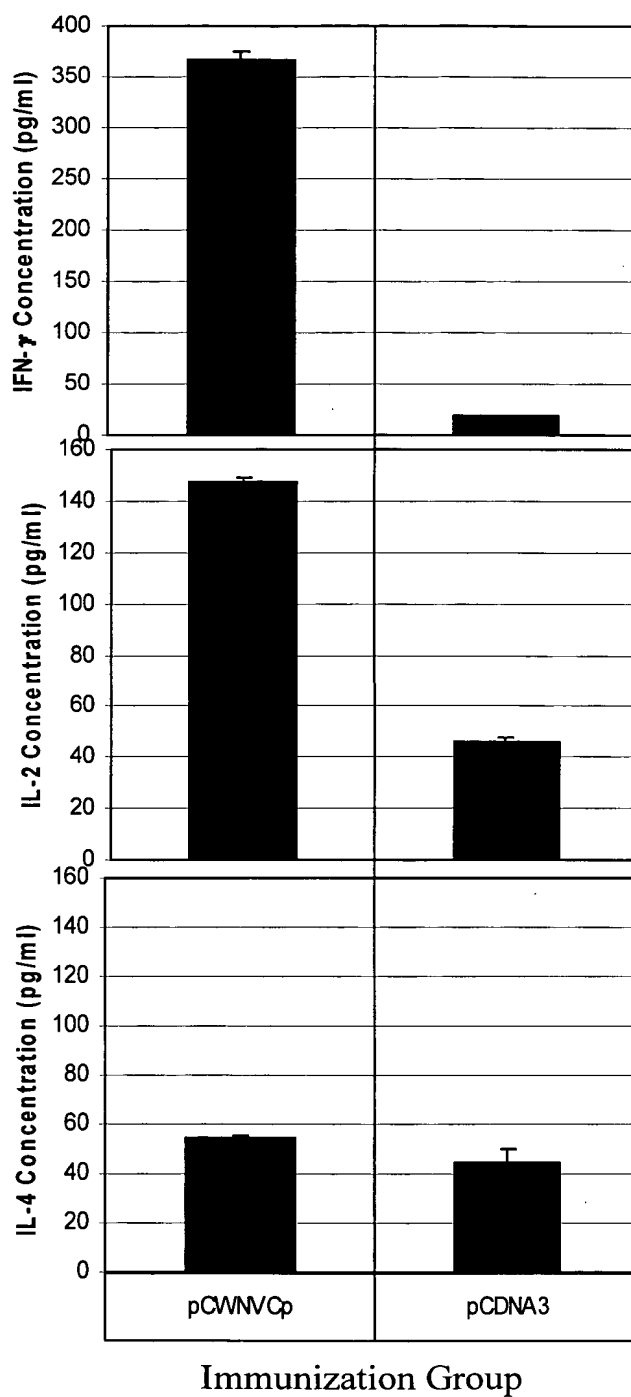


Figure 13

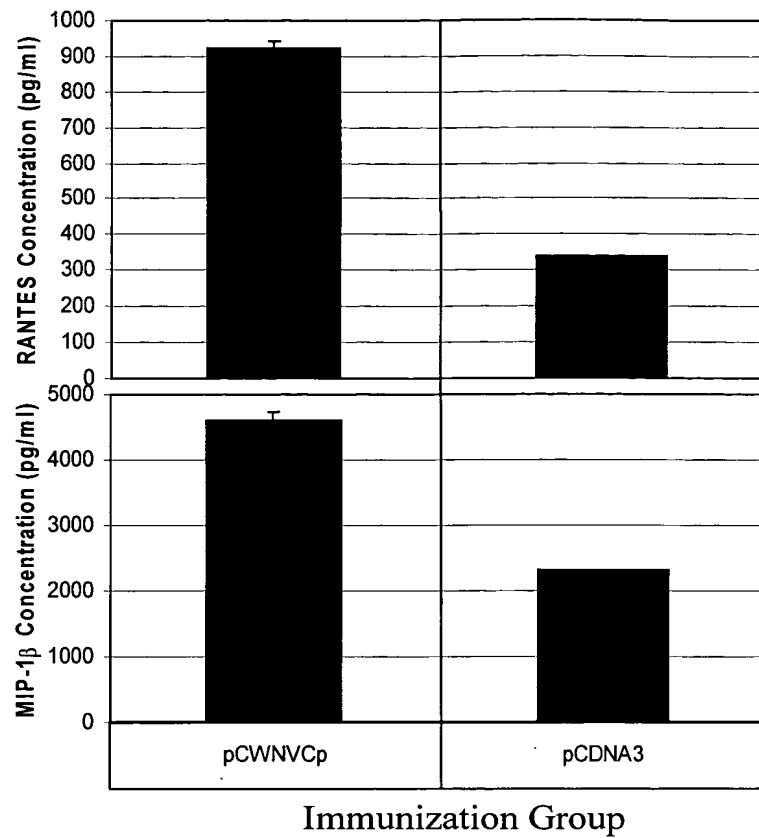


Figure 14

Fig. 15A

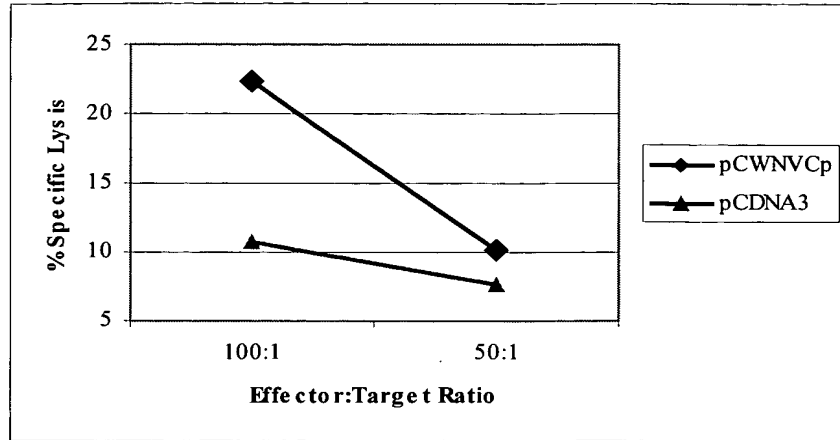


Fig. 15B

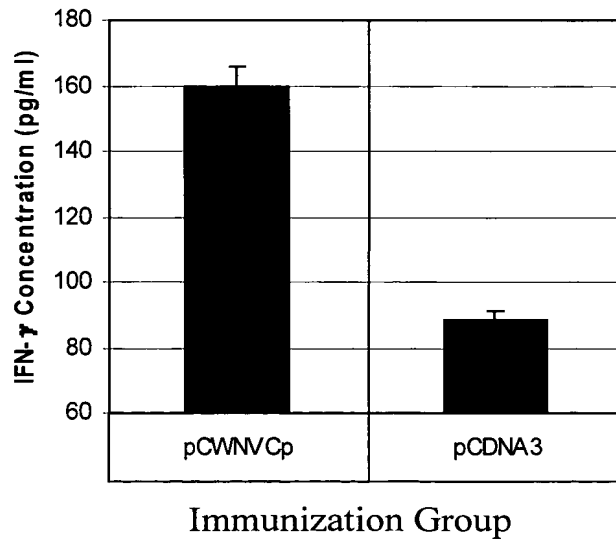


Fig. 16A

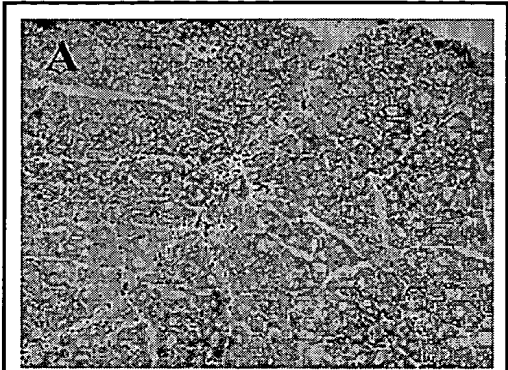


Fig. 16B

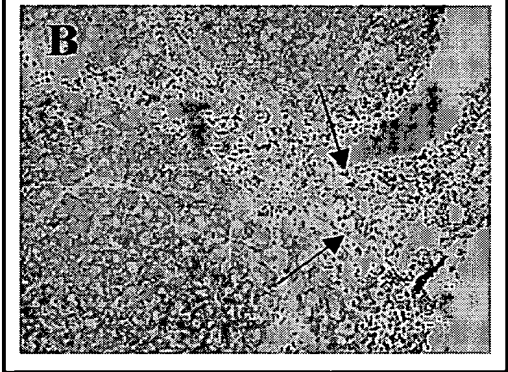


Fig. 16C

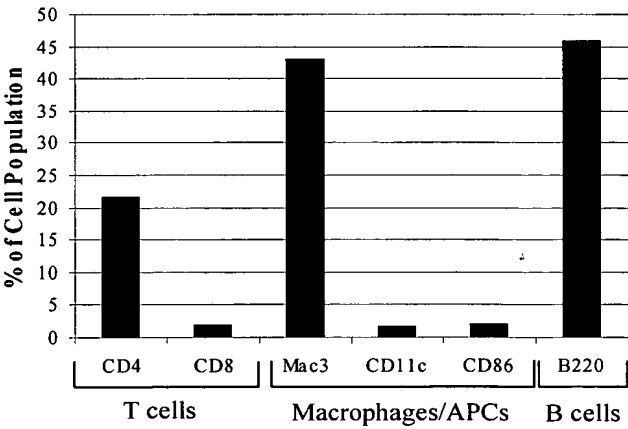
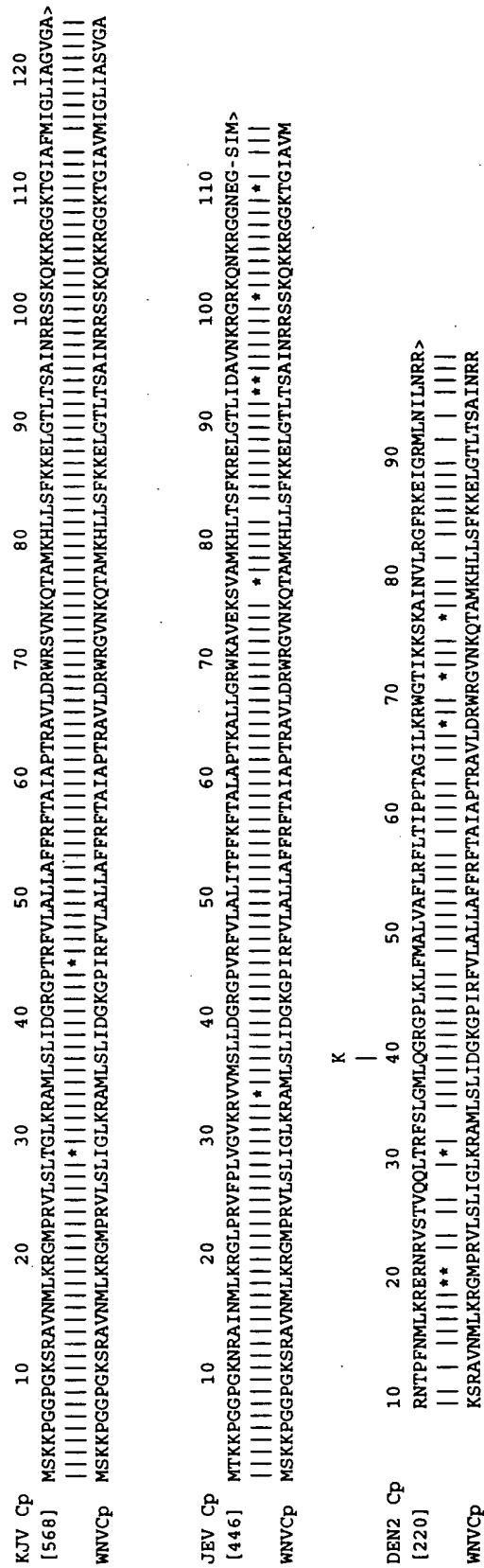


Figure 17



Year	1970	1971	1972	1973	1974	1975	1976	1977	1978	1979	1980	1981	1982	1983	1984	1985	1986	1987	1988	1989	1990	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099	2100
1970	1971	1972	1973	1974	1975	1976	1977	1978	1979	1980	1981	1982	1983	1984	1985	1986	1987	1988	1989	1990	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099	2100	

Database: UserFolder: Alignment-AC6/01

1. HIV-1 89.6 Vpr protein
1. HIV-1 89.
[41]
WNVcAa

[illegible][illegible]

4. Ebola glycoprotein
 4. EbolaGlyc 120 130
 [30] KPDGSECLPAAPDGIRGFPR>
 WNVc aa KPGGPGKSRVNNMLKGMPR

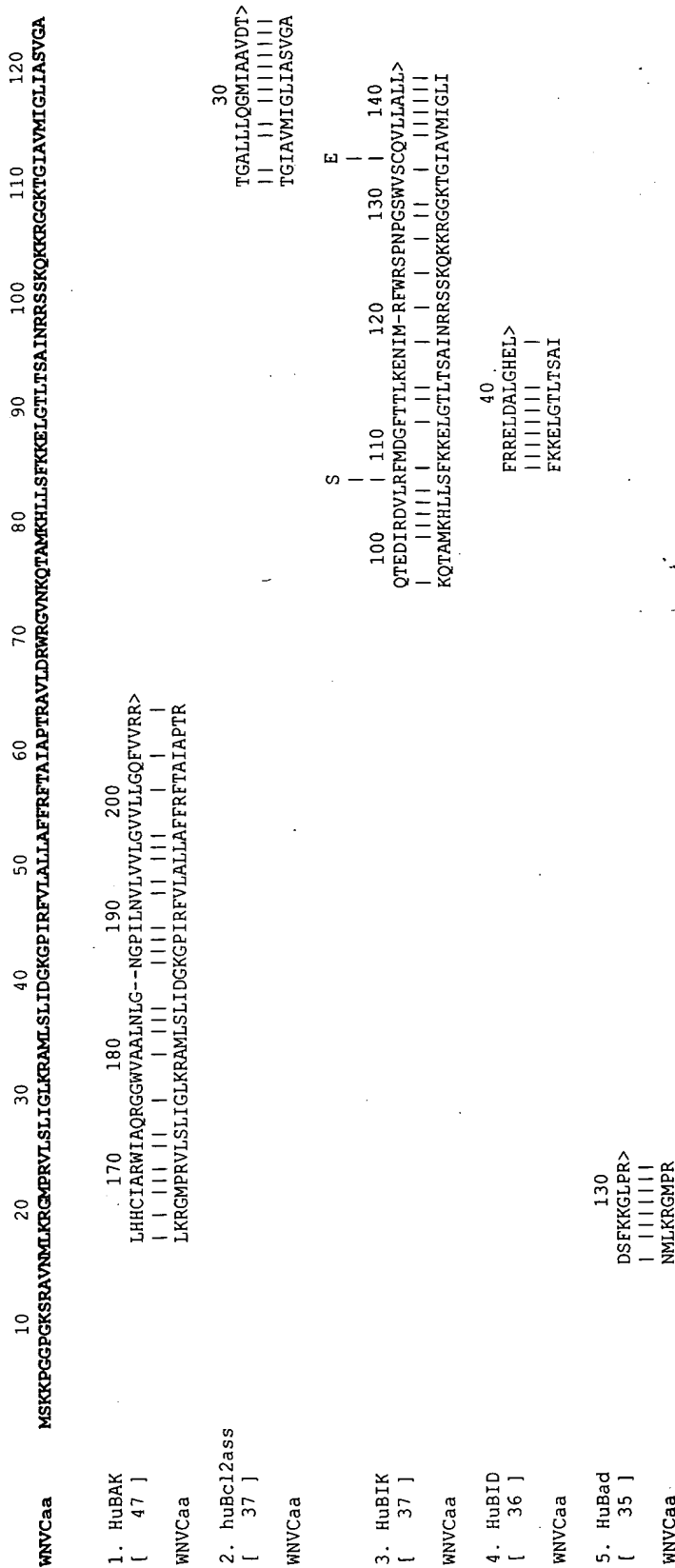
5. Ebola glycoprotein
 5. EbolaGlyc
 [39]
 WNVc aa

6. Rubella capsid protein
 6. Rubellaca
 [38]
 WNVc aa

570 580 590
 LQLELRATTELRTEFSLNRK-AID>
 LLAFFRFTAIAPTRAVLDRWGVN

270 280 290 300 310
 RSARHPWRI-R-FGAPQAFAG-LLLATVAVGTAR-AGLQP-RADMAAPPIL>
 RAVLDRWGVNKTAMKHLISFKELGTLTSAINRRSSKQKRGKGTGIAM

Year	1950	1951	1952	1953	1954	1955	1956	1957	1958	1959	1960	1961	1962	1963	1964	1965	1966	1967	1968	1969	1970	1971	1972	1973	1974	1975	1976	1977	1978	1979	1980	1981	1982	1983	1984	1985	1986	1987	1988	1989	1990	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099	2100
1950	1951	1952	1953	1954	1955	1956	1957	1958	1959	1960	1961	1962	1963	1964	1965	1966	1967	1968	1969	1970	1971	1972	1973	1974	1975	1976	1977	1978	1979	1980	1981	1982	1983	1984	1985	1986	1987	1988	1989	1990	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099	2100	



Search Analysis for Sequence: HIV-1 89.6 VpraaMatrix: pam250 matrix
 Search from 1 to 96 where origin = 1
 Date: June 15, 2001
 Time: 19:57:09
 Score Region from 1 to 96
 Maximum possible score: 515

HIV-1 89.6 MEQAPEDCGPQREPYNDWTLLEELLEELKNEAVRHPRIWLHSLGHIYETQDWTGVEALIRILQQLLFTFRTCGRHSRIGIIQORRTNGASKS

		1320	1330	1340
1. p230nonst	{ 50 }			
		FRQLDNRSTQFTPHLNCVSSVYEG--T-RDGVGA>		
HIV-1 89.6		LEELKNEAVRHFPPRIWLHSLGQHIIYETYGDWTGTVEA		

2. WNV Caa
[45]

HIV-1 89.6

```
RWRGVNKQTA-MKLLSFKELGTLTSAINRRSSKQKRGGTG>
|||||      |||      |      |      |      |
TWTVGEALIRILQOLLFTHFRIGCRHSRIGIIQQRRRTNGASKS
```

3. Cumbermos
[36]
IV-1 89.6

4. **Cucumovirus 2A protein**

4. Cumbermos
 [40]

HIV-1 89.6

110 120
 EFGNTSEVDDPLR-EVORL>
 |||| | ||| ||||
 TYGDTWTGVEALIRILQQL

5. **Rubella virus capsid protein**

5. Rubellaca
 [33]

HIV-1 89.6

160
 WLMSECGAVFY>
 |||| | ||
 RIWLHSLGQHIY

6. **Nipah virus fusion protein**

6. NipahFusi
 [44]

HIV-1 89.6

.sky.sd...vf->
 | | | | | | |
 LIRILQQLFIHF

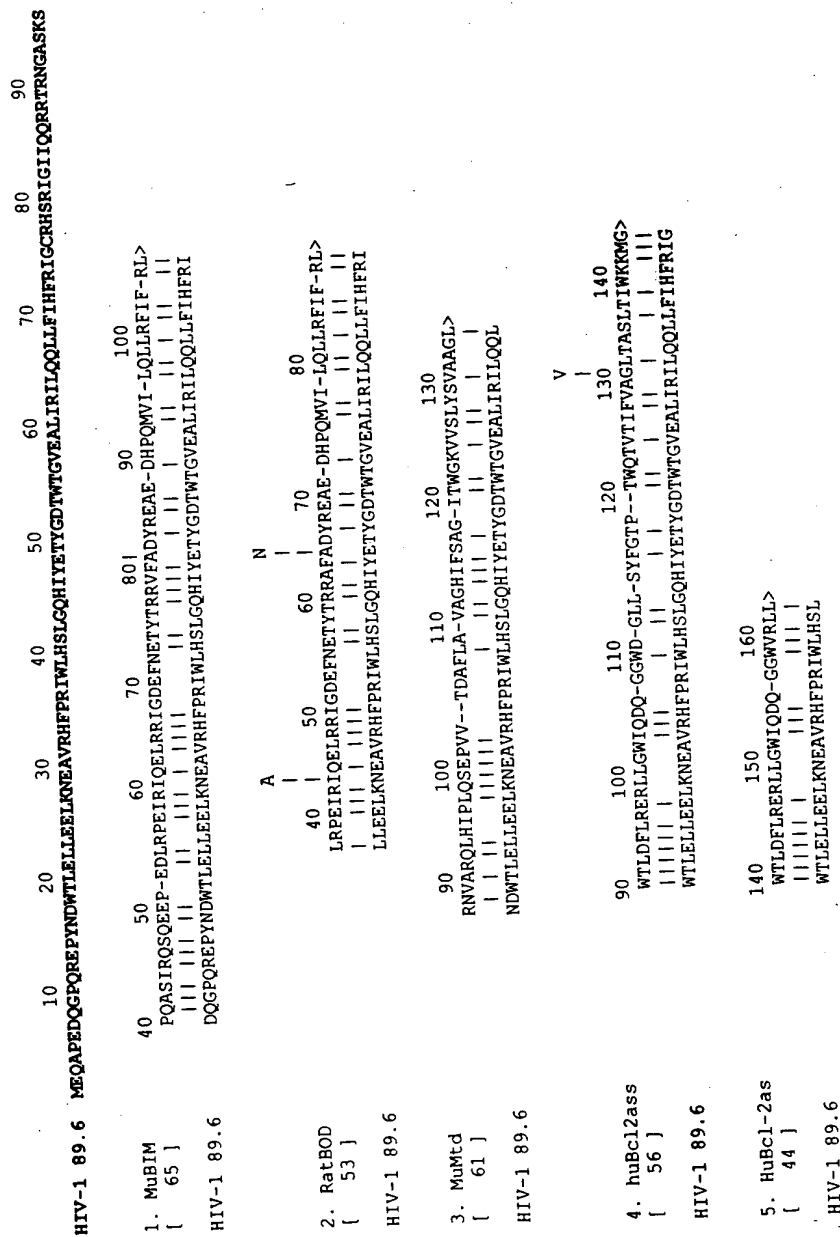
7. **Reovirus core-minor form Mu2**

7. Minor-Reo 410 420 430
 [46] IGAVLPKGSFKSTIMRVLDEMEVLGVRIMPR>

HIV-1 89.6

EDQGFQREPYNDWTLELLEELKNEAVRHFPR
 | | | | | | |
 | | | | | | |

Fig. 19 (continued) Alignment of HIV-1 89.6 Vpr protein sequence to proapoptotic proteins



150 160
VFQSWDRNLGR>
| | | | |
HFPRWLHSLGQ

6. HuBad
[36]
HIV-1 89.6